

Sun Oct 22 12:45:53 2000

us-08-894-356c-21.rpr

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GenCore version 4.5
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OM protein - protein search, using SW model

Run on: October 20, 2000, 01:34:22 ; Search time 11.52 seconds
(without alignments)
33,052 Million cell updates/sec

Title: US-08-894-356c-21

Perfect score: 40

Sequence: 1 DFGCK 6

Scoring table:

BLOSUM62
Gapop 10.0, Capext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR.65:
2: PIR.1:
3: PIR.3:
4: PIR.4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	443	2	T45574 anthranilate N-hyd
2	40	100.0	450	2	T45573 anthranilate N-hyd
3	40	100.0	451	2	T00527 hypothetical prote
4	40	100.0	455	2	T09666 probable anthranil
5	40	100.0	460	2	T03274 har201 protein, hy
6	40	100.0	461	2	T00918 hypothetical prote
7	40	100.0	461	2	T45961 anthranilate N-ben
8	36	90.0	475	2	T46216 anthranilate N-ben
9	35	87.5	442	2	T10718 anthranilate N-ben
10	35	87.5	445	2	T10717 anthranilate N-ben
11	35	87.5	445	2	T10719 anthranilate N-ben
12	35	87.5	446	2	T10711 anthranilate N-ben
13	35	87.5	445	2	T33865 anthranilate N-ben
14	35	87.5	572	2	T10056 hypothetical prote
15	34	85.0	113	2	S30578 wound-induced prot
16	34	85.0	129	2	S60978 probable membrane
17	34	85.0	216	2	T02913 hypothetical prote
18	34	85.0	519	2	S24300 transketolase (EC
19	34	85.0	667	2	G69723 transketolase-like
20	34	85.0	734	2	T47886 response regulato
21	33	82.5	730	2	A15486 hypothetical prote
22	32	80.0	234	2	T36369 response regulato
23	32	80.0	299	2	T16787 24-sterol C-methyl
24	32	80.0	346	2	T10173 probable 24-sterol
25	32	80.0	367	2	T19688 hypothetical prote
26	32	80.0	409	2	T48008 hypothetical prote
27	32	80.0	428	2	T48008 hypothetical prote
28	31	77.5	106	2	B64350 hypothetical prote
29	31	77.5	110	1	F71129 hypothetical prote

30	31	77.5	110	2	F75034	hypothetical prote
31	31	77.5	112	2	JU0131	biophenyl-2,3-diol
32	31	77.5	158	2	S35201	serine proteinase
33	31	77.5	215	2	G70342	hypothetical prote
34	31	77.5	261	2	S74761	hypothetical prote
35	31	77.5	291	1	B53419	biophenyl-2,3-diol
36	31	77.5	293	1	DAPSIC	biophenyl-2,3-diol
37	31	77.5	296	2	JW0103	azarene castazole
38	31	77.5	299	2	A28718	biophenyl-2,3-diol
39	31	77.5	299	2	A57264	2,3-dihydroxybiphe
40	31	77.5	316	2	T31282	sugar-phosphate de
41	31	77.5	316	2	F69978	hypothetical prote
42	31	77.5	335	2	T48319	alcohol dehydrogen
43	31	77.5	371	2	B69502	urophosphoryl-II C
44	31	77.5	393	2	S02185	mannose-6-phosphat
45	31	77.5	412	2	T40155	

ALIGNMENTS

RESULT 1
T45574
anthranilate N-hydroxycinnamoyl/phenyltransferase-like protein - Arabidopsis thaliana
N/Alternate names: protein P1C1.120
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence, revision 04-Feb-2000 #text, change 04-Feb-2000
R/Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Maves, H.W.;
submitted to the Protein Sequence Database, December 1999
A/Reference number: 233007
A/Accession: T45574
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-443 <BAR>
A/Cross-references: EMBL:AL132976
A/Experimental source: cultivar Columbia; BAC clone P1C1
C/Genetics:
A/Map position: 3
A/Note: P1C1.120

Query Match
Best Local Similarity 100.0%: Score 40; DB 2; Length 443;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DFGCK 6
DB 386 DFGCK 391

RESULT 2

T45573

anthranilate N-hydroxycinnamoyl/phenyltransferase-like protein - Arabidopsis thaliana
N/Alternate names: protein P1C1.110
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence, revision 04-Feb-2000 #text, change 04-Feb-2000
R/Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Maves, H.W.;
submitted to the Protein Sequence Database, December 1999
A/Reference number: 233007
A/Accession: T45573
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-450 <BAR>
A/Cross-references: EMBL:AL132976
A/Experimental source: cultivar Columbia; BAC clone P1C1
C/Genetics:
A/Map position: 3
A/Note: P1C1.110

Query Match 100.0%: Score 40; DB 2; Length 450;

Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 391 DRGWCK 396

RESULT 3

T00527
Hypothetical protein T20K24.8 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Apr-1999

C:Accession: T00527

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997

A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.

A:Reference number: 214167

A:Accession: T00527

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-451 <R0U>

A:Cross-references: EMBL:AC003393; NID:93176701; PID:93176709

A:Experimental source: cultivar Columbia

A:Genetics:

A:Map position: 2

A:Introns: 322/1

A:Note: T20K24.8

Query Match 100.0%; Score 40; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 8.9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 397 DRGWCK 402

RESULT 4

T09666

probable anthranilate N-benzoyltransferase (EC 2.3.1.144) - muskmelon (fragment)

N:Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase

C:Species: Cucumis melo (muskmelon)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C:Accession: T09666

R:Aggelis, A.; John, I.; Karvouni, Z.; Grierson, D.

Plant Mol. Biol. 33, 313-322, 1997

A:Title: Characterization of two cDNA clones for mRNAs expressed during ripening of melo

A:Reference number: 216810; MID:97188564

A:Accession: T09666

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-455 <RAG>

A:Cross-references: EMBL:Z70521; NID:0991794; PID:0334032

A:Experimental source: cultivar Cantaloupe charantais; pericarp of ripe fruit

C:Keywords: acyltransferase; coenzyme A

Query Match 100.0%; Score 40; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 374 DRGWCK 379

RESULT 5

T03274

har201 protein, hypersensitivity-related - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 07-May-1999

C:Accession: T03274

R:Czernek, P.; Huang, H.C.; Marco, Y.

Plant Mol. Biol. 31, 255-265, 1996

A:Title: Characterization of har201 and har515, two tobacco genes preferentially expr

A:Reference number: 214876; MID:96343929

A:Accession: T03274

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-460 <CZD>

A:Cross-references: EMBL:X05343; NID:91171576; PID:0220213

A:Experimental source: cultivar bottom special

C:Genetics:

A:Gene: har201

Query Match 100.0%; Score 40; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 382 DRGWCK 387

RESULT 6

T00918

hypothetical protein F21B7.32 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999

C:Accession: T00918

R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.;

et al.; submitted to the EMBL Data Library, January 1998

A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.

A:Reference number: 214208

A:Accession: T00918

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-461 <SHD>

A:Cross-references: EMBL:AC002560; NID:92618677; PID:92809263; GSPDB:GN00059; ATSP:F2

A:Gene: ATSP:F21B7.32

A:Map position: 1

Query Match 100.0%; Score 40; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 400 DRGWCK 405

RESULT 7

T45961

anthranilate N-benzoyltransferase-like protein - Arabidopsis thaliana

N:Alternate names: protein F7J8.190

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T45961

R:Beran, M.; Zimmermann, W.; Gruenleisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.;

submitted to the Protein Sequence Database, January 2000

A:Reference number: 223018

A:Accession: T45961

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-475 <BEV>

A:Cross-references: EMBL:AL137189

A:Experimental source: cultivar Columbia; BAC clone F7J8

C:Genetics:

A:Map position: 5

A:Note: F7J8.190

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XX      MO9625500-A1.
PM
XX      22-AUG-1996.
PD
XX      16-FEB-1996; 96MO-JP00348.
PF
XX      30-JAN-1996; 96JP-0046534.
PR      17-FEB-1995; 95JP-0067159.
PR      29-JUN-1995; 95JP-0196915.
XX      (SUNR ) SUNTORX LTD.
XX      Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
PI      Nakao M, Tanaka Y, Yonekura K;
DR      WPI: 1996-393401/39.
DR      N-PSDB: W04724.
XX
XX      DNA coding for aromatic acyl transferase - for transforming plants
PT      which produce anthocyanin pigments and thus altering colour tone,
PR      e.g. of flowers
XX
XX      Claim 4: Page 61-65; 94pp: Japanese.
PS
XX      Vectors containing DNA fragments encoding proteins of plant origin
CC      with aromatic acyl transferase activity may be used to transform
CC      plants which produce anthocyanin pigments. The aromatic acyl
CC      transferase acylates the pigments in the flower resulting in colour
CC      tone changes and allowing new colourations to be produced. Six
CC      specific DNA sequences encoding aromatic acyl transferase from
CC      different plants are described in T37308-T37313.
XX
SQ      Sequence 448 AA;

Query Match          100.0%; Score 40; DB 17; Length 448;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRGNCR 6
DB      390 dfgw9k 395

RESULT 7
W04727
ID      W04727 standard; Protein: 450 AA.
XX
AC      W04727;
XX
XX      06-FEB-1997 (first entry)
DE      Aromatic acyl transferase of Lavandula angustifolia.
XX
XX      Aromatic acyl transferase; transformation: anthocyanin pigment;
KM      plants; acylation; colour; tone; colouration; colour change;
KM      Gentiana triflora; Petunia hybrida; Perilla ocimoides;
KM      Senecio cruentus; Lavandula angustifolia.
XX
OS      Lavandula angustifolia (clone plant1).
XX
XX      Key
PM      Location/Qualifiers
PT      Misc-difference 1 /note= "Unidentified amino acid"
XX
XX      W09625500-A1.
PM
XX      22-AUG-1996.
PD
XX      16-FEB-1996; 96MO-JP00348.
PF
XX      30-JAN-1996; 96JP-0046534.
PR

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PR      17-FEB-1995; 95JP-0067159.
PR      29-JUN-1995; 95JP-0196915.
XX
XX      (SUNR ) SUNTORX LTD.
XX
XX      Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
PI      Nakao M, Tanaka Y, Yonekura K;
DR      WPI: 1996-393401/39.
XX
XX      DNA coding for aromatic acyl transferase - for transforming plants
PT      which produce anthocyanin pigments and thus altering colour tone,
PR      e.g. of flowers
XX
XX      Claim 4: Page 73-76; 94pp: Japanese.
PS
XX      Vectors containing DNA fragments encoding proteins of plant origin
CC      with aromatic acyl transferase activity may be used to transform
CC      plants which produce anthocyanin pigments. The aromatic acyl
CC      transferase acylates the pigments in the flower resulting in colour
CC      tone changes and allowing new colourations to be produced. Six
CC      specific DNA sequences encoding aromatic acyl transferase from
CC      different plants are described in T37308-T37313. NOTE: This
CC      sequence is supposed to cross reference with the nucleotide
CC      described in T37313, however there are so many discrepancies between
CC      the polypeptide decoded from that sequence and this polypeptide
CC      given in the specification that the indexer decided not to cross
XX      reference the two.
XX
SQ      Sequence 450 AA;

Query Match          100.0%; Score 40; DB 17; Length 450;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRGNCR 6
DB      393 dfgw9k 398

RESULT 8
W04726
ID      W04726 standard; Protein: 454 AA.
XX
AC      W04726;
XX
XX      06-FEB-1997 (first entry)
DE      Aromatic acyl transferase of Senecio cruentus.
XX
XX      Aromatic acyl transferase; transformation: anthocyanin pigment;
KM      plants; acylation; colour; tone; colouration; colour change;
KM      Gentiana triflora; Petunia hybrida; Perilla ocimoides;
KM      Senecio cruentus; Lavandula angustifolia.
XX
OS      Senecio cruentus (clone pcAr8).
XX
XX      W09625500-A1.
XX
XX      22-AUG-1996.
PD
XX      16-FEB-1996; 96MO-JP00348.
PF
XX      30-JAN-1996; 96JP-0046534.
PR      17-FEB-1995; 95JP-0067159.
PR      29-JUN-1995; 95JP-0196915.
XX
XX      (SUNR ) SUNTORX LTD.
XX
XX      Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
PI      Nakao M, Tanaka Y, Yonekura K;

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